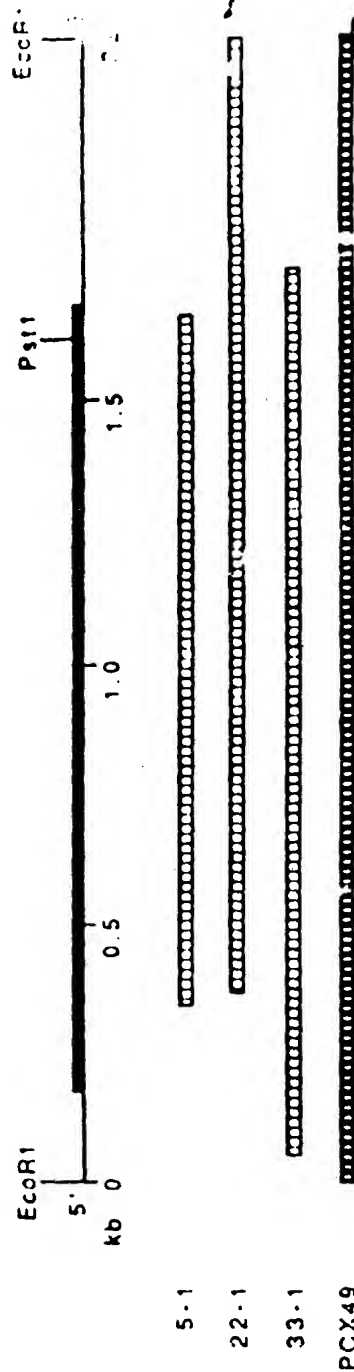


FIG. 1

FIG. 7A



1/321384

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10 30 50
 GGC ACC GGG GCG CCG CCG CTC CTC CTA CTC CTC CTC CTC CTA GGG ACC GGC
 Gly Thr Gly Ala Pro Pro Pro Leu Leu Leu Leu Pro Leu Leu Leu Leu Leu Gly Thr Gly
 70 90 110
 CTC TTC CCT GCT AGC AGC CAC ATA GAG ACC GCG GCC CAT GCG GAG GAG GCG CTC CTC AAC
 Leu Leu Pro Ala Ser Ser His Ile Glu Thr Arg Ala His Ala Glu Glu Arg Leu Leu Lys
 130 150 170
 AGA CTC TTC TCC GGT TAC AAC AAG TGG TCT CCG CCA GTA GCG AAT ATC TCA CAT CTC CTC
 Arg Leu Phe Ser Gly Tyr Asn Lys Trp Ser Arg Pro Val Gly Asn Ile Ser Asp Val Val
 190 210 230
 CTC GTC GCG TTT GCG TTC TCC ATT GCT CAG CTC ATT GAC GTC GAC GAG AAC AAC CAG ATC
 Leu Val Arg Phe Gly Leu Ser Ile Ala Gln Leu Ile Asp Val Asp Glu Lys Asn Gln Met
 250 270 290
 ATC ACA ACC AAC GCG TGG GTC AAG CAG GAG TGG CAC GAC TAC AAC CCG GCG TGG GAC CCT
 Met Thr Thr Asn Val Trp Val Lys Gln Glu Trp His Asp Tyr Lys Leu Arg Trp Asp Pro
 310 330 350
 GGT GAC TAC GAG AAT GTC ACC TCC ATC GCG ATC CCC TCT GAA CTC ATC TGG AGG CCT GAC
 Gly Asp Tyr Glu Asn Val Thr Ser Ile Arg Ile Pro Ser Glu Leu Ile Trp Arg Pro Asp
 370 390 410
 ATC GTC CTC TAC AAC AAT GCG GAT GGA GAC TTT GCA GTC ACC CAC CTC ACC AAC GCC CAC
 Ile Val Leu Tyr Asn Asn Ala Asp Gly Asp Phe Ala Val Thr His Leu Thr Lys Ala His
 430 450 470
 CTC TTC TAT GAC GGA AGG GTC CAG TGG ACA CCC CCA GCC ATC TAT AAG AGC TCC TGC AGC
 Leu Phe Tyr Asp Gly Arg Val Gln Trp Thr Pro Pro Ala Ile Tyr Lys Ser Ser Cys Ser
 490 510 530
 ATC GAC GTC ACC TTC TTC CCG TTT GAC CAG CAG AAC TGT ACC ATG AAG TTT GGA TCC TGG
 Ile Asp Val Thr Phe Phe Pro Phe Asp Gln Gln Asn Cys Thr Met Lys Phe Gly Ser Trp
 550 570 590
 ACC TAC GAC AAG GCC AAG ATT GAC TTA GTC AGC ATT CAT AGC CCG GTC GAC CAA CTC GAC
 Thr Tyr Asp Lys Ala Lys Ile Asp Leu Val Ser Ile His Ser Arg Val Asp Gln Leu Asp
 610 630 650
 TTC TGG GAA AGT GCG GAG TGG GTC ATC GTC CAT GCT GTC GCG ACC TAC AAC ACC AGG AAG
 Phe Trp Glu Ser Gly Glu Trp Val Ile Val Asp Ala Val Gly Thr Tyr Asn Thr Arg Lys
 670 690 710
 TAC GAG TGC TGT GCC GAG ATC TAT CCT GAC ATC ACC TAT GCG TTC ATC ATC CCA GCG CCG
 Tyr Glu Cys Cys Ala Glu Ile Tyr Pro Asp Ile Thr Tyr Ala Phe Ile Ile Arg Arg Leu
 730 750 770
 CCG CTA TTC TAC ACC ATC AAC CTC ATC ATC CCG TGC CTC CTC ATC TCC TGT CTC ACC GCG
 Pro Leu Phe Tyr Thr Ile Asn Leu Ile Ile Pro Cys Leu Leu Ile Ser Cys Leu Thr Val

FIG. 2A(1)

#/321354

790 810 830
 CTG CTC TTC TAT CTG CCT TCA GAG TGT GGC GAG AAG CTC ACA CTC TCC ATC TGC GTC CTG
 Leu Val Phe Tyr Leu Pro Ser Glu Cys Gly Glu Lys Val Thr Leu Cys Ile Ser Val Leu

850 870 890
 CTT TCT CTC ACC GTC TTC CTG CTG ATC ATC ACC GAG ATC ATC CCG TCC ACT TGC CTC CTC
 Leu Ser Leu Thr Val Phe Leu Leu Leu Ile Thr Glu Ile Ile Phe Ser Thr Ser Leu Val

910 930 950
 ATC CCG CTC ATC GGC GAG TAC CTC CTC TTC ACC ATC ATC TTC CTC ACC CTC TCC ATC GTC
 Ile Pro Leu Ile Gly Glu Tyr Leu Leu Phe Thr Met Ile Phe Val Thr Leu Ser Ile Val

970 990 1010
 ATC ACC GTC TTC GTC CTC AAT GTC CAC CAC CCG TCC CCA CCG ACA CAC ACC ATC CCG GCG
 Ile Thr Val Phe Val Leu Asn Val His His Arg Ser Pro Arg Thr His Thr Met Pro Ala

1030 1050 1070
 TCG GTC CCG AGA GTC TTC CTG GAG ATC GTC CCG CCG CTC CTC TTC ATC AAG CCG CCG TCT
 Trp Val Arg Arg Val Phe Leu Asp Ile Val Pro Arg Leu Leu Phe Met Lys Arg Pro Ser

1090 1110 1130
 GTC CTC AAA GAC AAC TGC CCG AGA CTT ATT GAG TCC ATC CAC AAG ATC GCG AAC GCG CCG
 Val Val Lys Asp Asn Cys Arg Arg Leu Ile Glu Ser Met His Lys Met Ala Asn Ala Pro

1150 1170 1190
 CCG TTC TCG CCA GAG CCT GTC GCG GAG CCG GCG ATC TTC AGT GAG ATC TCG AAC CAA CCG
 Arg Phe Trp Pro Glu Pro Val Gly Glu Pro Gly Ile Leu Ser Asp Ile Cys Asn Gln Gly

1210 1230 1250
 CTG TCA CCG GCC CCA ACT TTC TGC AAC CCC ACC GAG ACA GCA GTC GAG ACC CAG CCG AGC
 Leu Ser Pro Ala Pro Thr Phe Cys Asn Pro Thr Asp Thr Ala Val Glu Thr Gln Pro Thr

1270 1290 1310
 TCG AGG TCA CCC CCG CTT GAG GTC CCT GAG TTG AAG ACA TCA GAG GTT GAG AAG GCG AGT
 Cys Arg Ser Pro Pro Leu Glu Val Pro Asp Leu Lys Thr Ser Glu Val Glu Lys Ala Ser

1330 1350 1370
 CCG TGT CCA TCG CCG GGC TCC TGT CCT CCA CCC AAG AGC AGC AGT GCG GCT CCA ATC CCG
 Pro Cys Pro Ser Pro Gly Ser Cys Pro Pro Pro Lys Ser Ser Ser Gly Ala Pro Met Leu

1390 1410 1430
 ATC AAA GCG AGG TCC CTG AGT GTC CAG CAT GTC CCC AGC TCC CAA GAA GCA GCA GAA GAT
 Ile Lys Ala Arg Ser Leu Ser Val Gln His Val Pro Ser Ser Gln Glu Ala Ala Glu Asp

1450 1470 1490
 GCG ATC CCG TGC CCG TCT CCG AGT ATC CAG TAC TGT GTT TCC CAA GAT GGA GCT GCG TCC
 Gly Ile Arg Cys Arg Ser Arg Ser Ile Gln Tyr Cys Val Ser Gln Asp Gly Ala Ala Ser

1510 1530 1550
 CCG GCT GAG AGC AAG CCG ACC AGC TCC CCG ACC TCC CTG AAG GCG CCG CCA TCC CAG CTT
 Leu Ala Asp Ser Lys Pro Thr Ser Ser Pro Thr Ser Leu Lys Ala Arg Pro Ser Gln Leu

FIG. 2A(2)

[Faint, illegible handwritten notes or bleed-through from the reverse side of the page.]

4-2 cDNA, 3' end

FIG. 2A(3)

ALPHA4.2 NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCE

... STGCATGACTA
-240

ATTAATCTCCGCCAGTTGTTTTCAGCCACACAGCGSACACGCGCCGACGCGCGCATCAAGTTGGGTGGGGGAGCTCTCGAGAGCGCAGCGCGGACAGCTGGTCAAGCGCCGCA

Met Glu Ile Gly Gly Pro Gly Ala Pro Pro Leu Leu Leu Leu Leu Leu Gly Tyr
 -20 -10
 GCCTGTATAGACCCCGCTCCGCTGCGCC
 ATC CAG ATC GCG GCG CCC CCC CCG CCG CTA CTC CTC CTA CCG ACC
 -40 -30
 -50

GCG CTC TTG CCT GCT ACC ACC CAC ATA CAG ACC CCG GCC CAT CCG CAG CAG CCG CTC CTC AAG ACA CTC TTC TCC GGT TAC AAC AAG TCC
 -1 1 10 30 60
 GCT Leu Leu Pro Ala Ser Ser Met Ile Glu Thr Arg Ala Met Ala Glu Glu Arg Leu Leu Phe Ser Gly Tyr Asn Lys Trp
 30

30 40 50
Ser Arg Pro Val Gly Asn Ile Ser Asp Val Leu Val Arg Phe Gly Leu Ser Ile Ala Glu Leu Val Asp Glu Lys Asn Glu
TCT CGC CCA GTA GGC AAT ATC TCA GAT GTG GTC CTC CAC TTT GCG TTG TCC ATT GCT CAG CTC ATT CAC GTG CAG AAC AAC CAG

[illegible]

	90	100	110
ATG	116	Pro Arg Lys Val Leu Tyr Asp Asn Ala Asp Gly Asp Phe Ala Val Thr Met Lys Ala	110
CAC	ATC CCC TCT GAA CTC ATC TAG AGG CCT GAG ATC CTC CTC TAC AAT CCG CAT GCA GAC TTG CCA CTC ACC CAC CTC ACC AAC GCC	300	
	270	300	330

120 130 140
 HIS LEU PHE TYR ASP GLY ARG VAL GLN TRP THR PRO ARG ALA ILE TYR LYS SER CYS SER ILE ASP VAL THR PHE PRO PHE ASP
 CAC CTC TTC TAT AAC GGA ARG GAG TGG ACA GGC CCA GCC ATC ATG AAC ACC TCC TGC ACC ATC GAC CTC ACC TTC CCC TTT GAC
 360 370 380 390 400 410 420

Gln Gln Asp Cys Thr Met Lys Phe Gly Ser Trp Thr Tyr Asp Lys Ile ASD Leu Val Ser Ile His Ser Arg Val Asp Gln Leu
CAG CAC CAG CAC TGT ACC ATG AAG TTT GUA TCC TGG ACC TAC CAC AAG ATT CAC TTA GTG AGC ATT CAT AGC GTG CAC CAA CTC
150 160 170

450 480 510

FIG. 2B(1J)

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180 Asp Phe Trp Glu Ser Gly Glu Trp Val Ile Val Asp Ala Val Gly Thr Tyr Asn Thr Arg Lys Tyr Glu Cys Arg Ala Glu Ile Tyr Pro
 CAC TTC TGG GAA ACT CGG GAG TGG GTC ATC ATC GTC GAT CCT GTC GGC ACC TAC AAC ACC AGG AAC TAC GAG TGC TGT GCC GAG ATC TAT CCT
 540 570 600
 210 Asp Ile Thr Tyr Ala Phe Ile Ile Arg Arg Leu Pro Leu Phe Tyr Thr Ile Asn Leu Ile Ile Pro Cys Leu Leu Ile Ser Cys Leu Thr
 GAC ATC ACC TAT GGC TTC ATC ATC GCA GGC GTC GCG CTA TTC TAC ACC ATC AAC CTC ATC ATC CCT TGC CTG CTC TGC TGT CTC ACC
 630 660 690
 240 Val Leu Val Phe Tyr Leu Pro Ser Glu Cys Gly Glu Lys Val Thr Leu Cys Ile Ser Val Leu Leu Ser Leu Thr Val Phe Leu Leu Leu
 CTG CTG GTC TTC TAT CTG CCT TCA GAG TGT GGC GAG AAG GTC ACA CTG TGC ATC TCG GTC CTG CTG TCT CTC ACC CTC TTC CTC CTG CTC
 720 750 780
 270 Ile Thr Glu Ile Ile Pro Ser Thr Ser Leu Val Ile Pro Leu Ile Gly Cys Tyr Leu Leu Phe Thr Met Ile Phe Val Thr Leu Ser Ile
 ATC ACC GAG ATC ATC CCG TCC ACC TCG CTC GTC ATC CCG CTC ATC GGC GAG TAC CTC CTC TTC ACC ATG ATC ATC TTC GTC ACC CTC TCC ATC
 810 840 870
 300 Val Ile Thr Val Phe Val Leu Asn Val His His Arg Ser Pro Arg Thr His Met Pro Ala Trp Val Arg Arg Val Phe Leu Asp Ile
 GTC ATC ACC GTC TTC GTC GTC AAT GTC CAC CAC GGC TCG CCA CAC ACA CAC ACG ATG CCG GGC TGG GTC GGT ACA GTC TTC CTC GAC ATC
 900 930 960
 330 Val Pro Arg Leu Leu Phe Met Lys Arg Pro Ser Val Val Lys Asp Asn Cys Arg Arg Leu Ile Glu Ser Met His Lys Met Ala Asn Ala
 CTG CCT GGC CTC CTC TTC ATC ATC AAG CCG CCC TCT GTC CTC AAA GAC AAC TGC CCG ACA CTT ATT GAG TCC ATG CAC AAG ATG GGC AAC GGC
 990 1020 1050
 360 Pro Arg Phe Trp Pro Glu Pro Val Gly Glu Pro Gly Ile Leu Ser Asp Ile Cys Asn Glu Glu Leu Ser Pro Ala Pro Thr Phe Cys Asn
 CCC GGC TTC TGG CCA GAG CCT GTC GGC GAG CCC GGC ATC TGC AGT GAC ATC TGC TGC AAC CAA GGT CTG TCA CCT GGC CCA ACT TTC TCC AAC
 1080 1110 1140
 390 Pro Thr Asp Thr Ala Val Glu Thr Glu Pro Thr Cys Arg Ser Pro Pro Leu Glu Val Pro Asp Leu Lys Thr Ser Val Glu Lys Ala
 CCC ACG GAC ACA GCA GTC GAG ACC CAG CCT ACG TCC ACG TCC CCG CTT GAG CTC GGT CCG GTC AAC ACA TCA GAG GTT GAG AAG GGC
 1170 1200 1230
 420 Ser Pro Cys Pro Ser Gly Ser Cys Pro Pro Lys Ser Ser Gly Ala Pro Met Leu Ile Lys Ala Arg Ser Leu Ser Val Glu
 ACT CCC TGT CCA TGG CCT GGC TCC TGT CCT CCA CCC AAG ACC ACG AGT GGG GGT CCA ATG CTC ATC AAA GCG ACG TCC CTC ACT GTC CAG
 1260 1290 1320

FIG. 2B(-)

[illegible]

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DATA DERIVED FROM:  CLONE AMIPDC  [JB]
                   CLONE AMYALI  [ESC]
```

28 MARCH 1988

FILED - 2015

FIG. 3(1)

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ALPHA4 FYTINLITFCLLISCLTVLVFYLPSIC
 ALPHA3 FYTINLITFCLLISCLTVLVFYLPSIC
 ALPHA1 YFIVNVIIIPCLLISCLTVLVFYLPSIC
 -----MSR I-----

ALPHA4 GERVTLCISVLLSLTVFLLLLITEIITIS
 ALPHA3 GERVTLCISVLLSLTVFLLLLITEIITIS
 ALPHA1 GERVTLCISVLLSLTVFLLLLITEIITIS
 -----MSR II-----

ALPHA4 TSLVIPLEICFYLLFTMHFVTLGIVITV
 ALPHA3 TSLVIPLEICFYLLFTMHFVTLGIVITV
 ALPHA1 TSSAVPLEICFYLLFTMHFVTLGIVITV
 -----MSR III-----

ALPHA4 FVLNVHHHSIMTHTMPA'WVPHVFLD'V
 ALPHA3 FVLNVHHHSIMTHTMPA'WVPHVFLD'V
 ALPHA1 FVLNVHHHSIMTHTMPA'WVPHVFLD'V

ALPHA4 PRLLEF - - - PKRFSVV(K)LNC(R)RLTESM
 ALPHA3 PRVMEF - - - MTHITSGEGDTPKT - - -
 ALPHA1 PNIMEFYSTMKHPSND(K)JERIR - - -

ALPHA4 KMANAPRFWPEPVGE'PGILSDICNOGL
 ALPHA3 - - - - - - - - - RTFYGAELSLNLCFSR
 ALPHA1 - - - - - - - - - TE'DIDISD'JSGKPG

ALPHA4 S(P)APT(F)CNPTDTAVE(T)OPT(C)KSPPLEV
 ALPHA3 ADSKSCKEGYPCQDG(T)CGY(CH)HRRVKI
 ALPHA1 P(P)PMCFH - - - - - - - - - - -

FIG. 3(2)

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ALPHA4	P D L K T S E V E X A S P C I S P G	[S] C P P P R [S] S S
ALPHA3	S N F - - - - -	[S] A N L T H S S S
ALPHA1	- - - - -	- - - - -

ALPHA4	G A P M L I K A R S L S V Q H V F S S Q L A A E D G I
ALPHA3	S E S V - - - - -
ALPHA1	- - - - -

ALPHA4	R C R S R S I Q Y C V S Q D G A A S L A D S K P T S S
ALPHA3	- - - - -
ALPHA1	- - - - -

ALPHA4	P T S L K A R P S Q L P V S D Q A S P C R C T C K E F
ALPHA3	- - - - -
ALPHA1	- - - - -

ALPHA4	S P V S P V T V L K A G C T R	[A] P P O H [L] P L S P A L
ALPHA3	- - - - -	- N [A] V L S L S A L S I E :
ALPHA1	- - - - -	- S P [L] I R H P E V

<-----

ALPHA4	T R [A] V [E] G V Q Y I A D H L [K] A E D T D F S V K [E] D W
ALPHA3	K E A I O S V K Y I A E N M K A O N V A K E I O D D W
ALPHA1	K S [A] I [E] G V K Y I A E T M K S D Q E S N N A A [E] F W

amphipathic helix----->

ALPHA4	K Y V A N V I D R I P L W M F I I V C L L G T V G L F
ALPHA3	K Y V A N V I D R I P L W V P I L V C I L G T A G L F
ALPHA1	K Y V A N V H D H I L L G V F M L V C L I G T L A V F

<----- KSR IV ----->

ALPHA4	[L] P P W L A C M I
ALPHA3	[L] O P L M A - R D D T
ALPHA1	A G R L I E L H Q Q G

-->

FIG. 3(3)

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FIG. 4A

Clone 4.1;
Antisense

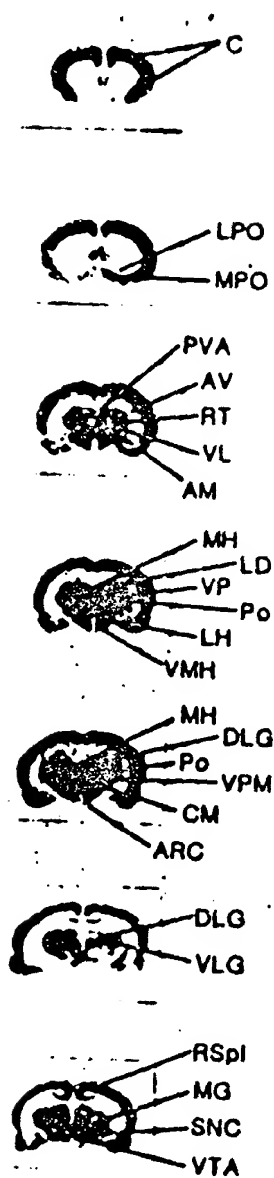
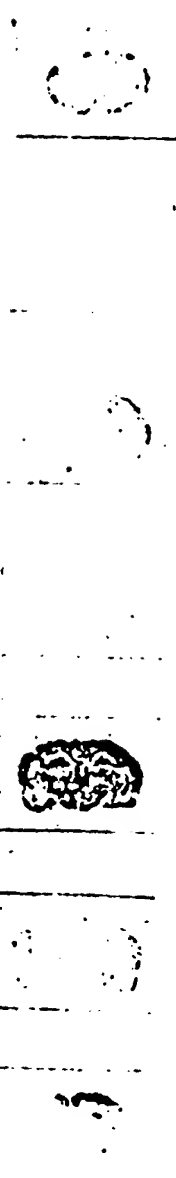


FIG. 4B

Clone 4.1;
Sense



07/321384

FIG. 5B

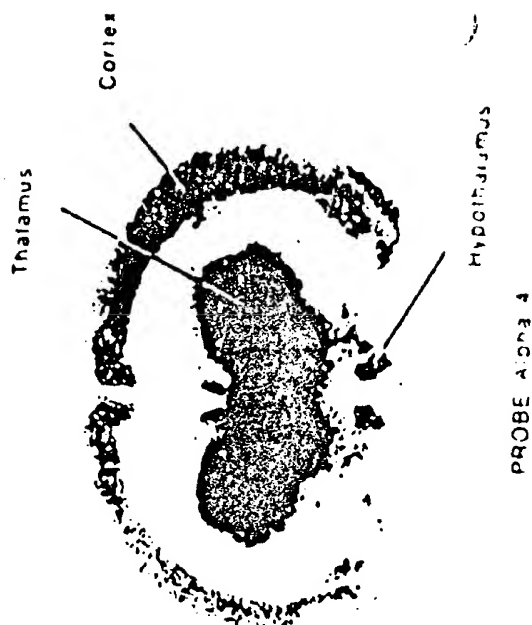
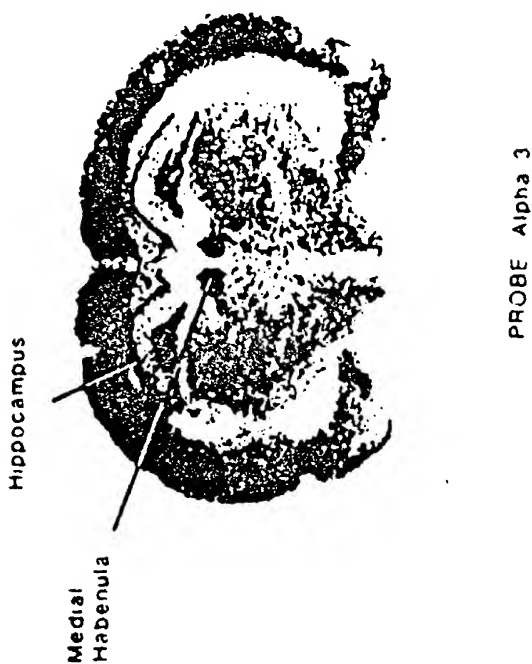
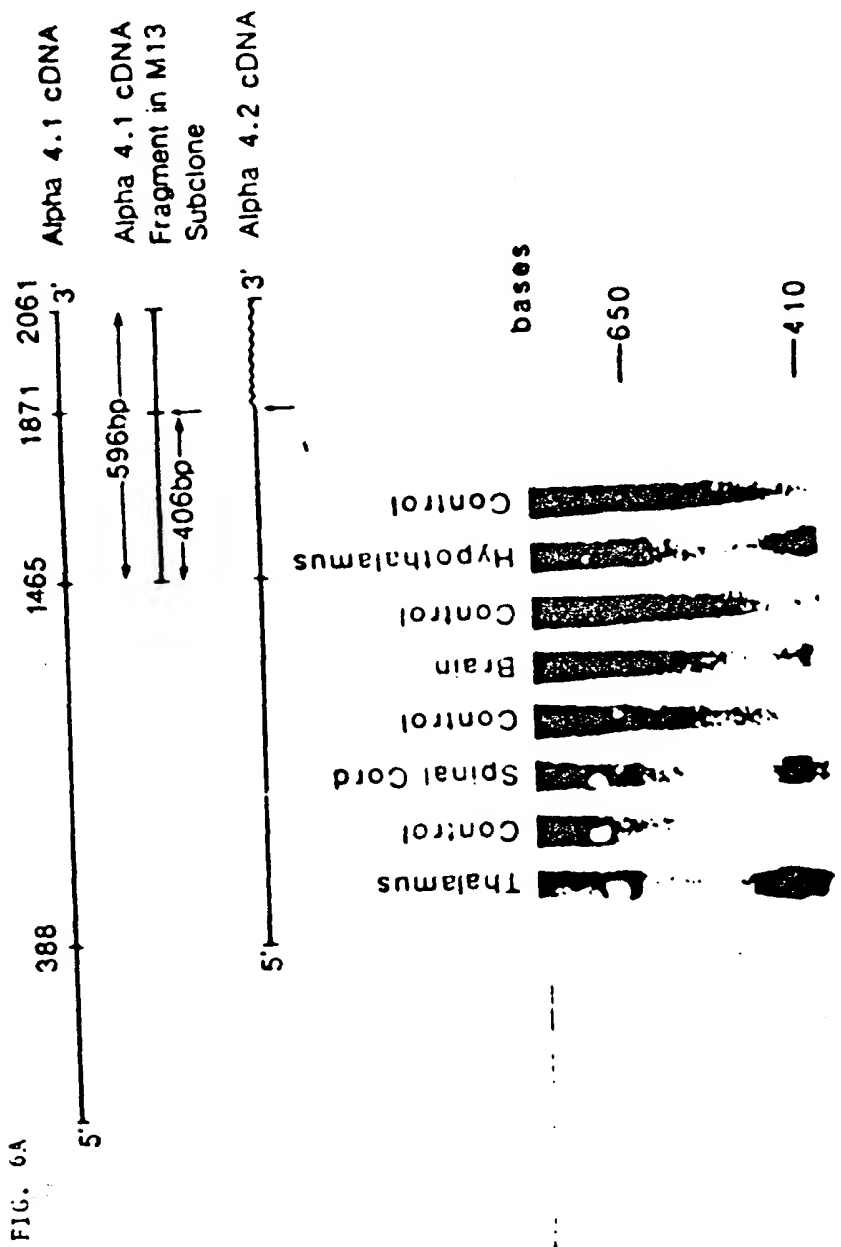


FIG. 5A





548
 TTT CCC TCA TCG ACC TAC GAC CGT ACT GAC ATT GAC CTG GTC AAA AGT CAT GTG GCC AGT CTG GAT CAC TTC
 Phe Arg Ser Trp Thr Tyr Asp Arg Thr Glu Ile Asp Leu Val Leu Lys Ser Asp Val Ala Ser Leu Asp Asp Phe
 178

600
 ACA CCC AGC GGG GAG TGG GAC ATC ATC GCA CTG CCA GGC CCA AAC GAG AAC CCA GAC TCC ACC TAT GTG
 Thr Pro Ser Gly Glu Trp Asp Ile Ile Ala Leu Pro Gly Arg Arg Asn Glu Asn Pro Asp Asp Ser Thr Tyr Val
 201

630
 GAC ATC ACC TAT GAC TTC ATC ATT CGT CCG AAA CCA CTC TTC TAC ACT ATC AAC CTC ATC ATC CCC TCC GTA CTC
 Asp Ile Thr Tyr Asp Phe Ile Ile Arg Arg Lys Pro Leu Phe Tyr Thr Ile Asn Leu Ile Ile Pro Cys Val Leu
 228

690
 ATC ACC TCG CTG GCC ATC CTG GTC TTC TAC TCC TCA GAC TGT GGT GAA AAG ATG ACA CTT TGT ATT TCT GTG
 Ile Thr Ser Leu Ala Ile Leu Val Phe Tyr Leu Pro Ser Asp Cys Gly Glu Lys Met Thr Leu Cys Ile Ser Val
 251

780
 CTG CTA GCA CTT GGT GTG TTC CTG CTC ATC TCC ACC ATT GTG CCG ACC TCC CTC CAT GTA CCG CTG CTG
 Leu Leu Ala Leu Thr Val Phe Leu Leu Leu Ile Ser Lys Ile Val Pro Pro Thr Ser Leu Asp Val Pro Leu Val
 278

840
 GGC AAG TAC CTC ATG TTT ACC ATG GTG CTA GTC ACC TTC TCC ATC CTC ACC AGC GTG TGT GTG CTC AAT GTG CAC
 Gly Lys Tyr Leu Met Phe Thr Met Val Leu Val Thr Phe Ser Ile Val Thr Ser Val Cys Val Leu Asn Val His
 301

890
 CAC CGC TCG CCT ACC XCG CAC ACC ATG GCC CCG TGG CTC AAG GTG GTC TTC CTG GAG AAG CTG CCC ACC CTC CTC
 His Arg Ser Pro Thr Thr Thr His Thr Met Ala Pro Trp Val Lys Val Val Phe Leu Glu Lys Leu Pro Thr Leu Leu
 328

930
 TTC CTG CAG CAG CCA CCG CAC CCG TGT GCA CGT CAG CGT CTC CCG TTC ACC AGC CC CAG CCA GAG CGT GAG GGC
 Phe Leu Gln Gln Pro Arg His Arg Cys Ala Arg Gln Arg Leu Arg Leu Arg Arg Arg Gln Arg Glu Arg Glu Gly
 351

2000

11

01/321384

2017

005250 29103500

FIG. 9A

—28S
—18S

FIG. 9B

1 2



28S—

18S—

11/321384

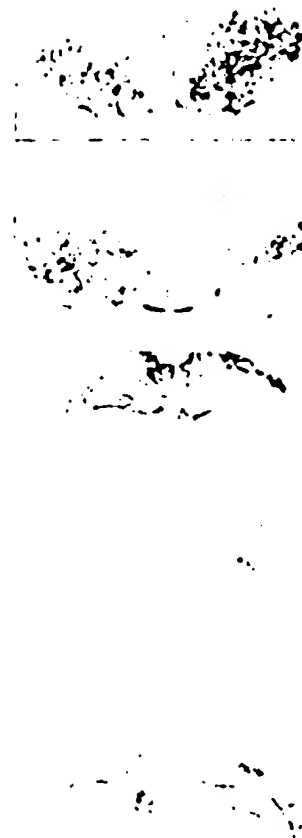
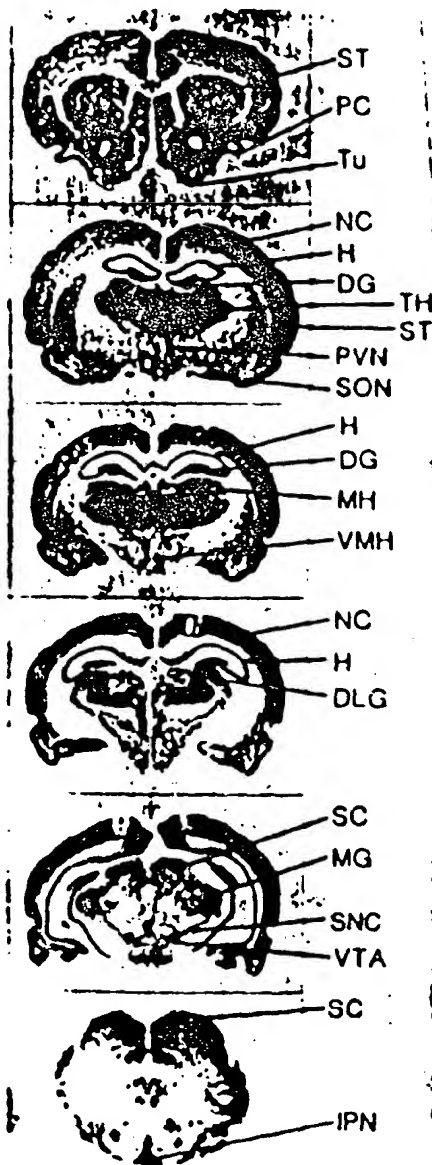
07/321384

FIG. 10A

FIG. 10B

ANTISENSE

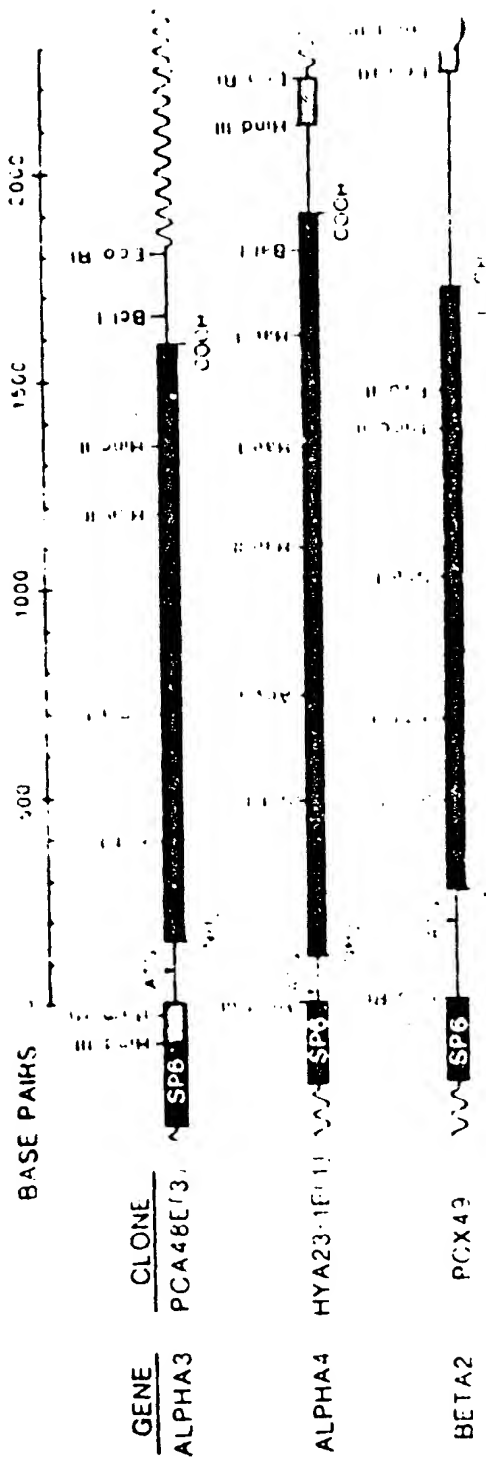
SENSE



ALPHA-SUBUNIT COMPOSITION

ALPHA 1
ALPHA 2
ALPHA 3
ALPHA 4
ALPHA 5
ALPHA 6
ALPHA 7
ALPHA 8
ALPHA 9
ALPHA 10
ALPHA 11
ALPHA 12
ALPHA 13
ALPHA 14
ALPHA 15
ALPHA 16
ALPHA 17
ALPHA 18
ALPHA 19
ALPHA 20
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ALPHA 94
ALPHA 95
ALPHA 96
ALPHA 97
ALPHA 98
ALPHA 99
ALPHA 100

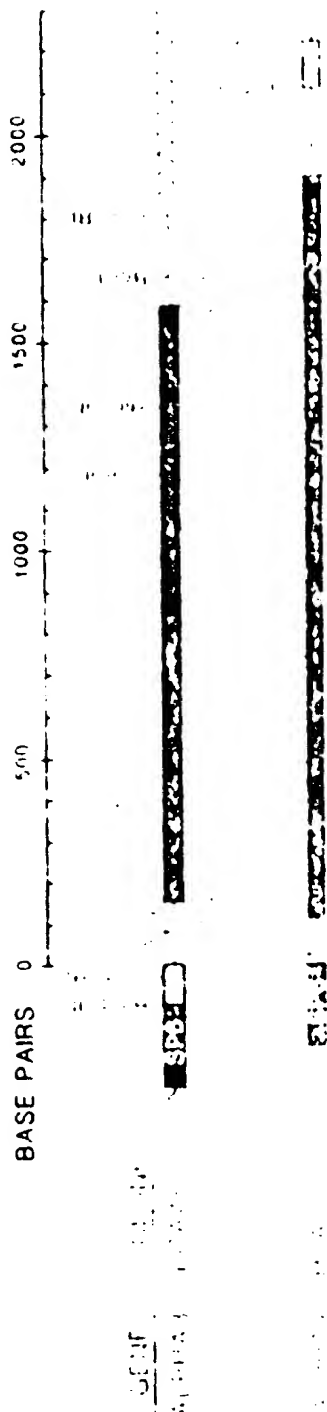
FIG. 12



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00550-230450

FIG. 12



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FIG. 12

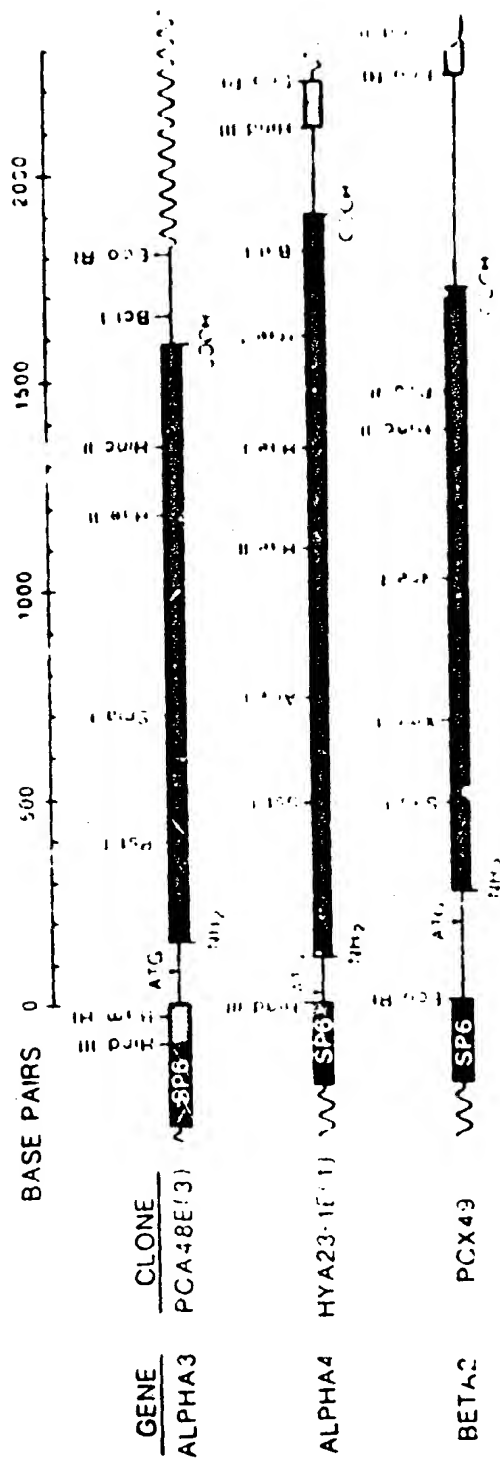
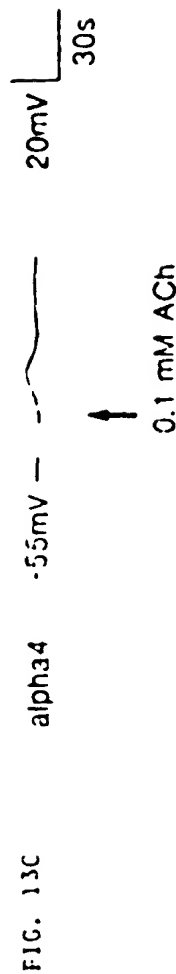
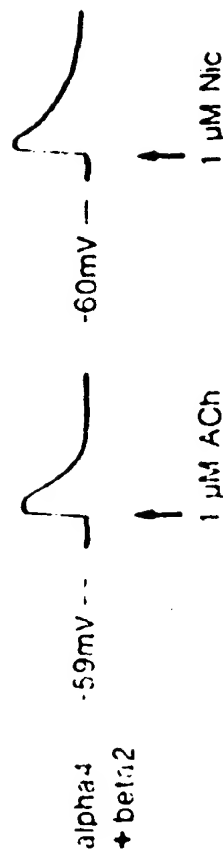
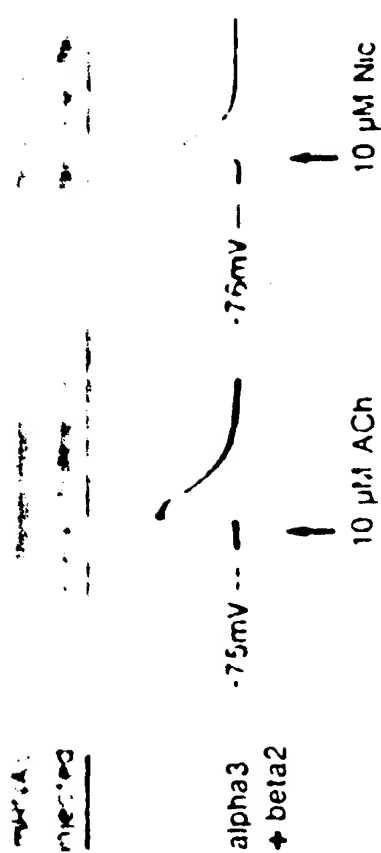


Diagram illustrating the structure of the $\alpha 3$, $\alpha 4$, and $\beta 2$ genes. The scale bar indicates base pairs (0 to 2000). The genes are labeled: **GENE** (ALPHA3, ALPHA4, BETA2) and **CLONE** (PCA48E13, HYA23-1E11, PCX49). The diagram shows the exon-intron structure and the positions of various restriction sites (EcoRI, BclI, HaeII, HhaI, PstI, HindIII, XbaI) and the 5' and 3' ends (ATG, CCGG).

CLONE PCA48513.

HYA23-1E-11

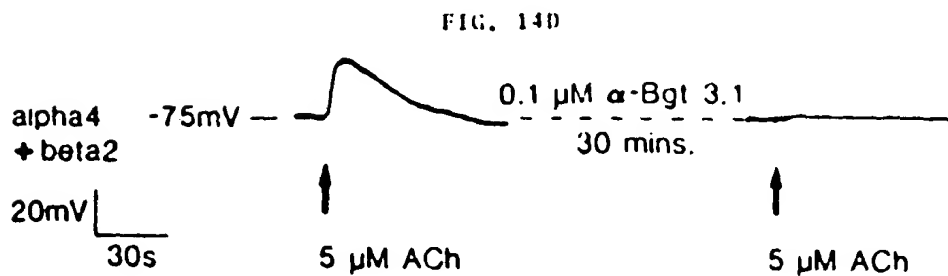
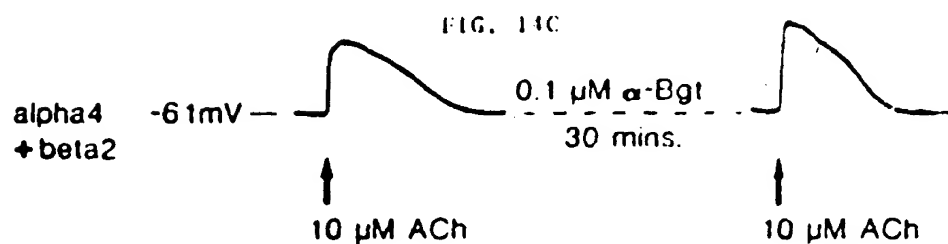
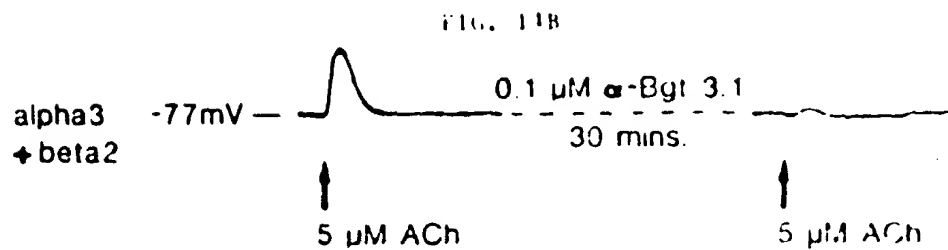
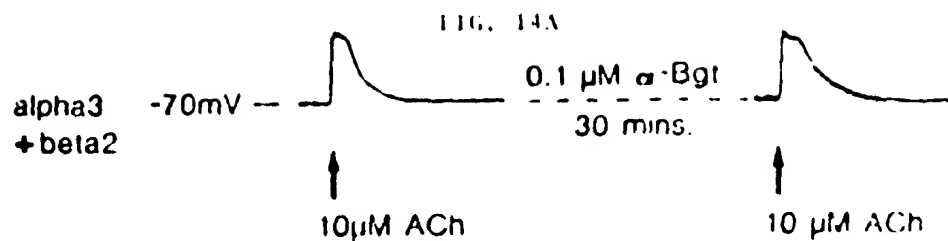
PCX49



mRNAs
injected

before toxin

after toxin

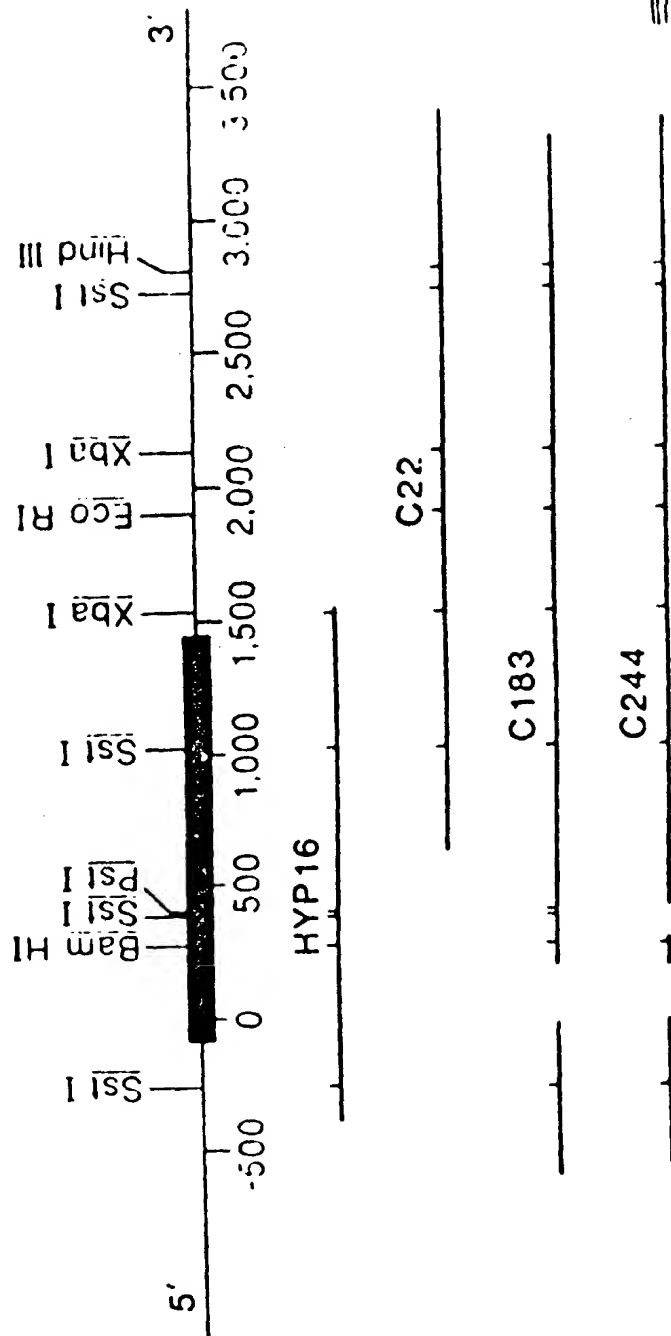


[illegible]

Q41

00550 2540500

FIG. 15B



07/321384

[illegible]

TGTTCAACTGGGATCACTCTATCTCCAGGAAGCTAGCCTGAATCCCTCATCTCCAACTGCTCTCCAAAGCTTTCCAGGTTCTCTCTCTCGGCAACATCATGCTCAAGCAACTGAGCTCTG
 -348 -338 -330 -278

-240
 TTCTTCACCTGTCACTGCTTCGAGCGACCCCTGCTCAGCCACCTCCAGGTCTCCACCGCGTTGGTTCTCTTCATGCAATTTCCAGCAGACAGT
 -210
 -180
 -150

-120
 -90
 -80
 -20
 -20

-38

TGG TGT CTC CTT CTC GTC CCA GCA G Gtaggt.....tatccacag TG TTG ACC CAG CAA GGC TCA CAC ACC CAT OCT CAC GAC CCC CTG TTT
Trp Cys Leu Leu Leu Val Pro Ala Y at Leu Thr Glu Glu Gly Ser His Ala Glu Asp Arg Leu P ;
-10 -1 -1 -1 38

68
A CAC CTG TTT GCA GGC TAC AAT CGC TGG GCA CGG CCA GTG CCC AAC ACT TCT CAT GTG GTC ATC GTG CGC TTT GCA TTA TCC ATT CCT
ys Mis Low Phe Gly Gly Tyr Asn Arg Trp Ala Arg Pro Val Pro Asn Thr Ser Asp Val Val Ile Val Arg Phe Gly Leu Ser Ile
20 20 30 30 40

150
 180
 60
 60

.....ccctggcgg G1A TCG AAT GAC TAC AAC CTG CCC TCG GAC CCG GCT GAG TTT CGC AAT GTC ACC TCC CTG CCG CTC CCT TCA GAG ATC
G1u Trp Asn Asp Tyr Lys cu Arg TTT Asp Pro A10 G1u Phe G1y Asn Val Thr Ser Leu Arg Val Pro Ser G1u Met
210 240 270 300

11.511

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Fig. 15c, d)

THE UNIVERSITY OF CHICAGO

1500 1530

116. 157.5

FIG. 17A

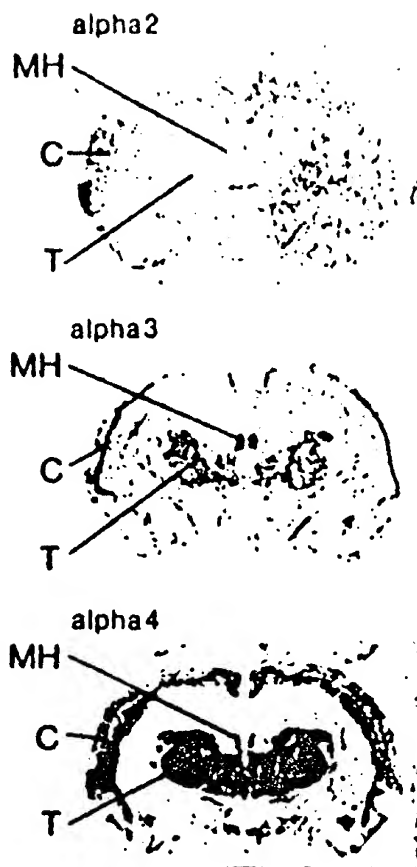
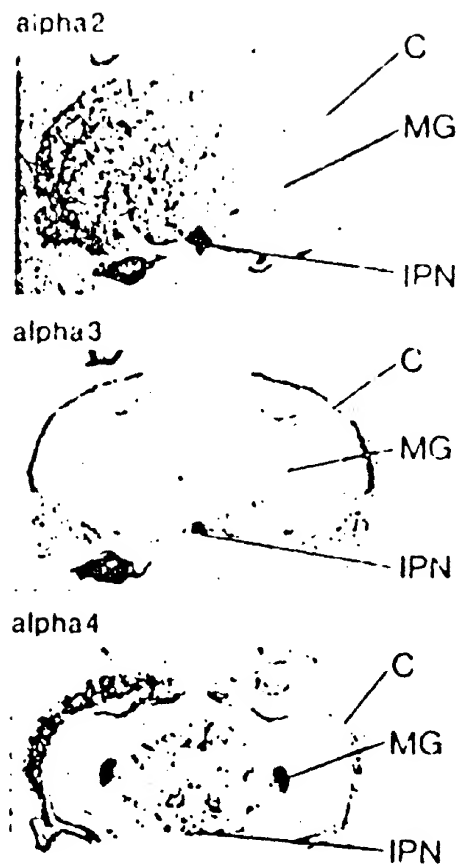
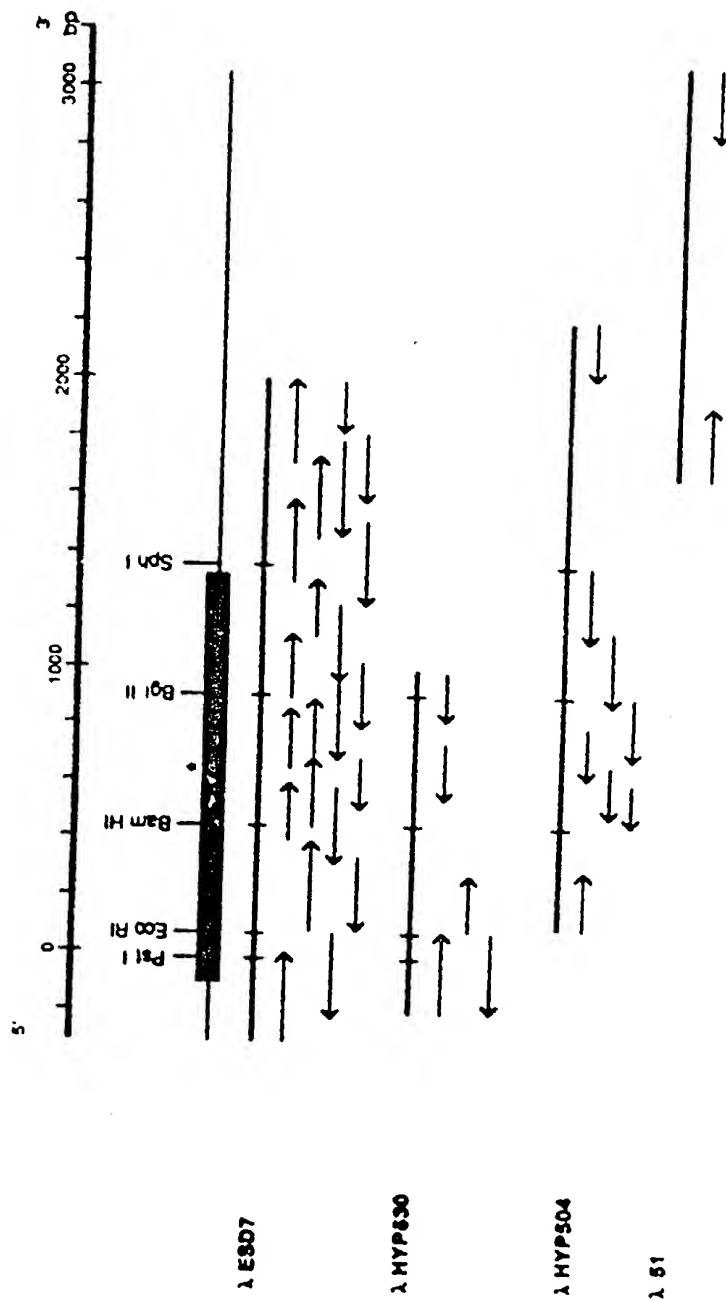


FIG. 17B



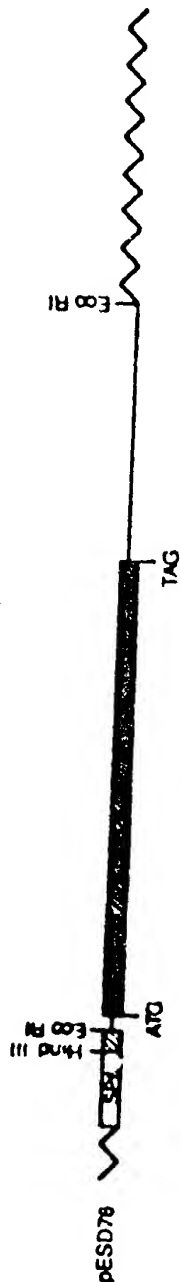
005250 29100560

FIG. 18A



00550-29102500

FIG. 18B



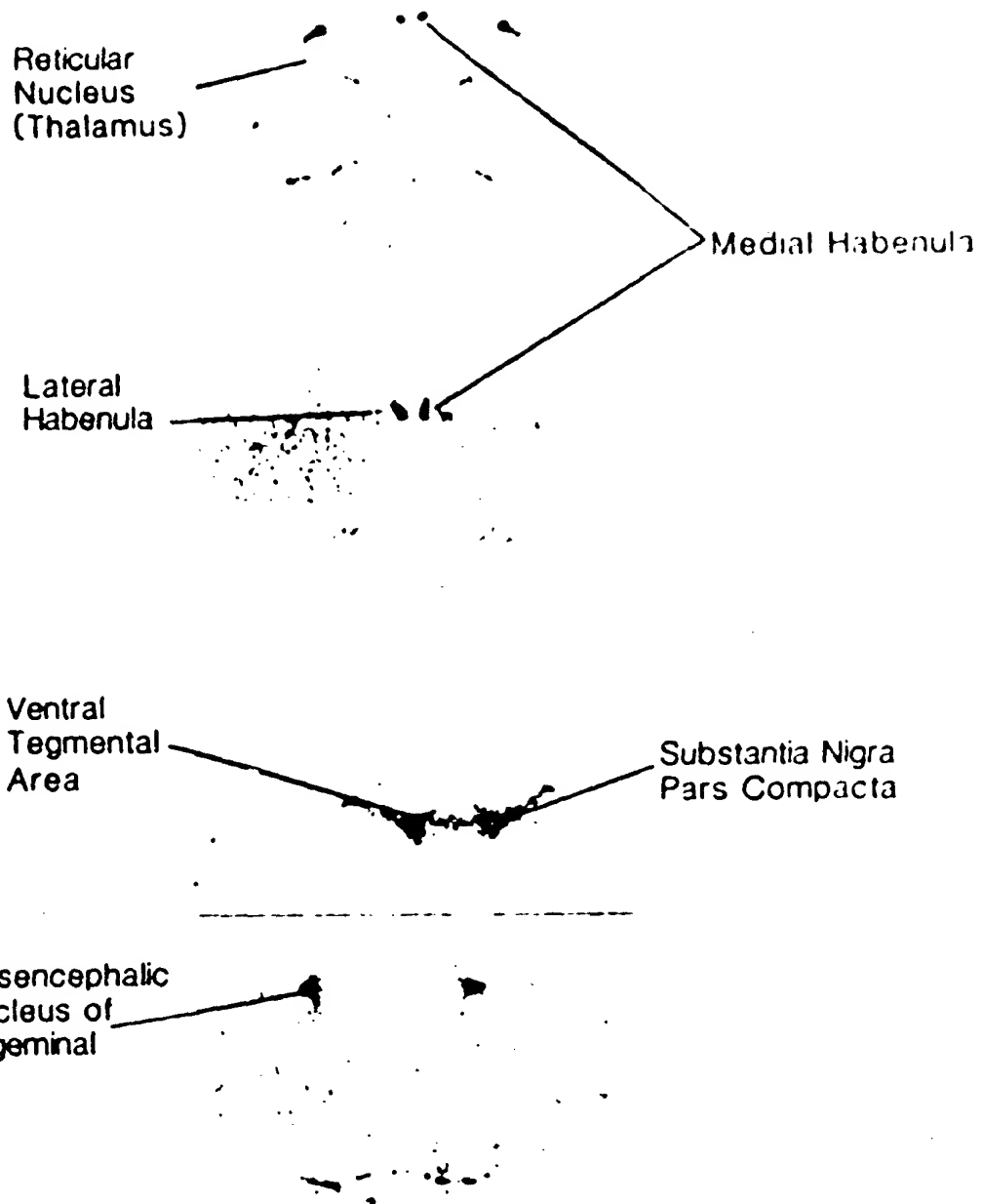
093562

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NEURONAL NICOTINIC ACETYLCHOLINE RECEPTOR SUBUNITS

BETA 3
 BETA 2
 ALPHA 2
 ALPHA 3
 ALPHA 4

FIG. 21



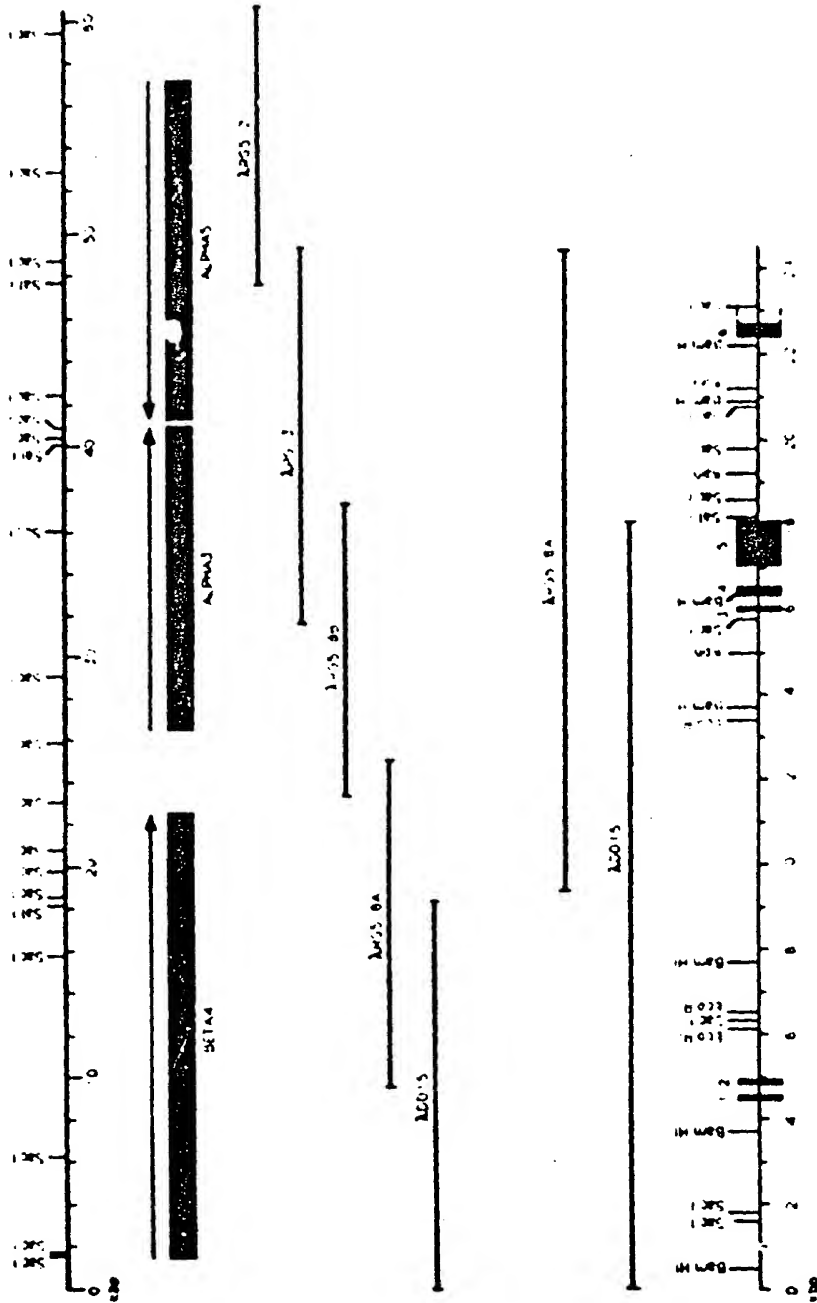
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116. 22

FIG. 23



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FIG. 24

100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000

ESC 755

FIG. 25

[illegible]

[illegible]

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FIG. 26

BTB#2 MLACHAGNSHMAHSPFSLMLWCSGVLTGOTTERLVELHLLDPBRYKHLIRPAPMGSELVTVOLMVLSLAOLIS:HEAEQ:MTTWLWLTQEMECYLI:IMPEPTEENR
BTB#3 MTGFLAVFLVSLATLSCSWYLTATAGLSVVAENHEDALLRHLPQCKYKWPVPLWSSDI:KVPFLKISQLOVDNFCNLTMTVLMWLCQEMWZQRLWHPPEEYGCN
BTB#4 MGTPTLLVLSLFLSLOLODCDCLANAEELMDOLLNTRNYNMLIRPAPSSSOLIS:IRLLLSLOLISVMRPEGIMTTSIMLWZEMWZQYLAHMSWSSCYLCVN

----- SIGNAL PEPTIDE -----

BETA2 KVALPSKRIMLPDVLYNNACHYEVSYFYSMAVSYSDS:FMLPPAIYKSAKRIEUVKPPFDPOOMCTNKRPSMT:RIEISVLKRSVA:LS:PP:PE:DL:AP:3
BETA3 STVPSLSMLPDLFVNADGAFESGLHTKAIYKSSVTSYPRASYKS:CHDV:TFPPAKONCMYF:SWTYS:DL:INEM:QKPFEMG:WEL:AS:G
BETA4 ILIRIPAKRV:PDIVLYNNACHYEVSYFYSMAVSYSDS:GLPPAIYKSAKRIEUVKPPFDPOOMCTNKRPSMT:RIEISVLKRSVA:LS:PP:PE:DL:AP:3
BETA5 ILIRIPAKRV:PDIVLYNNACHYEVSYFYSMAVSYSDS:GLPPAIYKSAKRIEUVKPPFDPOOMCTNKRPSMT:RIEISVLKRSVA:LS:PP:PE:DL:AP:3

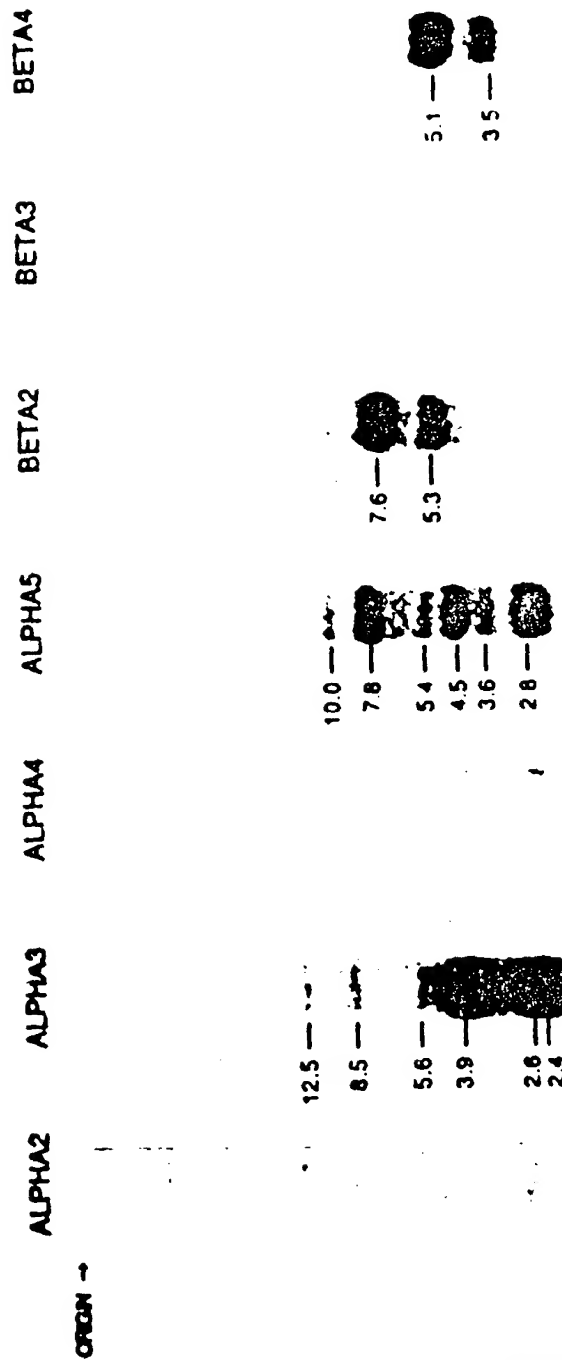
BETA2 RNNENPODS TYVDITYDPIIRKRPFTYTNLIIPCVLTISLAILUTYDLYDSGCEPMTCTISLIALTVLTLVLTWVUPPTSELEVAVGVPFMTLTPFTRFTR
 BETA3 MKGNRRGEGFYSPITYSVLRKRPFTYTNLIIPCVLTISLAILUTYDLYDSGCEPMTCTISLIALTVLTLVLTWVUPPTSELEVAVGVPFMTLTPFTRFTR
 BETA4 RRIVNPOOP SYVDUTYDPIIRKRPFTYTNLIIPCVLTISLAILUTYDLYDSGCEPMTCTISLIALTVLTLVLTWVUPPTSELEVAVGVPFMTLTPFTRFTR

[illegible][illegible]

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FIG. 28



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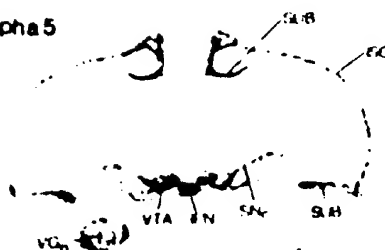
07/321384

FIG. 29

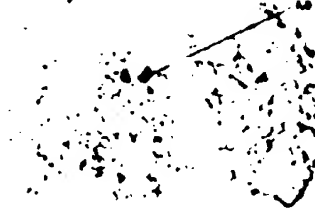
alpha 5



alpha 5



beta 4



083915